

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wolf, Marcia K
Cassels, Fred J
Boedeker, Edgar C
- (ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Assoc
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: VA
 - (E) COUNTRY: US
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/479,877
 - (B) FILING DATE: 10-JAN-2000
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna M
 - (B) REGISTRATION NUMBER: 32,535
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703/425-8405
 - (B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTGTA	CCAGTTGATA	AAAATATATC	ACGCTGGGAA	TGACGTGATG	TATATACGGA	60
GCAGCTATGT	CGGAACAGAT	ATTTTCCTAT	CGGTATGCGT	TGTGAGTAAG	CGTAAAGCCA	120
ATGCTGTCTG	TAACTCCTGA	TCCTTGCAGA	CTAAATTAGA	GCTCCTTCTA	AATTAGACGG	180
ATGGATAAAC	CTACAGACTG	GCGCTCTGGG	TCTCGCCGGA	TATTTTCTAA	TGAATTTAAG	240
CTTCATATGG	TTGAACTGGC	TTCGAAACCA	AATGCCAATG	TCGCACAAC	GGCTCGGGAA	300
CATGGCGTTG	ATAACAACCT	GATTTTTTAA	TAGCTACGCC	TCTGGCAAAG	AGAAGGACGT	360
ATTTCTCGTA	GAATGCCTCC	AACTATTGTA	GGCCCTACAG	TACCACTGAG	GTAGCCTGAA	420
TTTAAAGCCG	AAGCGGTCAG	AACTGTTCTT	GGTGTGAACG	TAGCACTCAC	CAATAAAAGC	480
ATCAATACGG	TGCTCTGTTG	ACACATTACG	AATGTTATGT	ATACAATAAA	AATGATTATA	540
GCAATATTAA	TGGTGTTATA	TGAAGAAAAC	AATTGGTTTA	ATTCTAATTC	TTGCTTCATT	600
CGGCAGCCAT	GCCAGAACAG	AAATAGCGAC	TAAAACTTC	CCAGTATCAA	CGACTATTTC	660
AAAAAGTTTT	TTTGCACCTG	AACCACGAAT	ACAGCCTTCT	TTTGGTGAAA	ATGTTGGAAA	720
GGAAGGAGCT	TTATTATTTA	GTGTGAACTT	AACTGTTTCT	GAAAATGTAT	CCCAGGTAAC	780
GGTCTACCCT	GTTTATGATG	AAGATTATGG	GTTAGGACGA	CTAGTAAATA	CCGCTGATGC	840
TTCCCAATCA	ATAATCTACC	AGATTGTTGA	TGAGAAAGGG	AAAAAATGT	TAAAAGATCA	900
TGGTGCAGAG	GTTACACCTA	ATCAACAAAT	AACTTTTAA	GCGCTGAATT	ATACTAGCGG	960
GGAAAAAAA	ATATCTCCTG	GAATATATA	CGATCAGGTT	ATGGTTGGTT	ACTATGTAAA	1020
CTAAATACTG	GAAGTATGAT	TATGTTGAAA	AAAATTATTT	CGGCTATTGC	ATTAATTGCA	1080
GGAACCTCCG	GAGTGGTAAA	TGCAGGAAAC	TGGCAATATA	AATCTCTGGA	TGTAAATGTA	1140
AATATTGAGC	AAAATTTTAT	TCCAGATATT	GATTCCGCTG	TTCGTATAAT	ACCTGTTAAT	1200
TACGATTCCG	ACCCGAAACT	GGATTACAG	TTATATACGG	TTGAGATGAC	GATCCCTGCA	1260
GGTGTAAGCG	CAGTTAAAA	CGCACCAACA	GATAGTCTGA	CATCTTCTGG	ACAGCAGATC	1320
GGAAAGCTGG	TTAATGTAAA	CAATCCAGAT	CAAAATATGA	ATTATTATAT	CAGAAAGGAT	1380
TCTGGCGCTG	GTAACTTTAT	GGCAGGACAA	AAAGGATCCT	TTCCTGTCAA	AGAGAATACG	1440
TCATACACAT	TCTCAGCAAT	TTATACTGGT	GGCGAATACC	CTAATAGCGG	ATATTCGTCT	1500

GGTACTTATG	CAGGAAATTT	GACTGTATCA	TTTACAGCA	ATTAAAAAA	GGCCGCATTA	1560
TTGCGGCCAT	TGACGATACT	GCTAGGCAAA	AATATGAAAT	CAAAGTTAAT	TATACTATTG	1620
ACGTTAGTGC	CATTTTCATC	TTTTTCAACA	GGAAATAATT	TTGAAATAAA	TAAGACACGA	1680
GTAATTTACT	CTGACAGCAC	ACCATCAGTT	CAAATATCAA	ATAATAAAGC	ATATCCTTTA	1740
ATTATTCAAA	GCAATGTATG	GGATGAAAGC	AATAATAAAA	ATCATGACTT	TATAGCAACA	1800
CCACCGATTT	TTAAAATGGA	AAGTGAAAGT	CGGAATATAA	TAAAAATAAT	TAAAACAAC	1860
ATTAATTTGC	CGGACTCTCA	GGAAAGTATG	AGATGGTTAT	GTATTGAATC	AATGCCACCA	1920
ATAGAAAAAA	GTACTAAAAT	AAACAGAAAA	GAAGGAAGGA	CAGACAGTAT	TAATATCAGC	1980
ATTCGGGGGT	GCATTAAACT	GATATATCGA	CCTGCCAGTG	TTCCGTCTCC	TGTTTTTAAT	2040
AATATAGTAG	AAAAATTAAA	ATGGCATAAA	AATGGAAAGT	ATCTTGTATT	AAAAATAAT	2100
ACACCCTATT	ACATTAGCTT	TTCTGAGGTT	TTTTTTGATT	CAGATAAAGT	AAACAATGCA	2160
AAAGATATTT	TATATGTAAA	ACCATACTCA	GAGAAGAAAA	TAGATATCAG	CAACAGAATA	2220
ATAAAAAAAA	TCAAATGGGC	TATGATTGAT	GATGCTGGCG	CAAAAACAAA	ACTTTATGAA	2280
TCAATTTTAT	AAAAATCTC	ATTACAGTAT	ACAAAAACAT	CAGATTACAG	GCTTGCTTTT	2340
TTTGCTATTT	ATATATCCTT	TCTCAACCTC	ATATGGAAAT	GAACAATTTA	GTTTTGACTC	2400
ACGATTCCTA	CCATCAGGTT	ATAATTACTC	TTTAAATAGT	AACTTACCTC	CTGAAGGTGA	2460
GTATCTGGTT	GATATTTATA	TTAACAAAAT	AAAAAAGGAG	TCCGCGATTA	TTCTTTTTTA	2520
TATAAAAGGA	AATAAACTTG	TACCATGTTT	ATCAAAAGAA	AAAATTTTCAT	CTTTGGGTAT	2580
CAACATTAAT	AATAACGACA	ACACAGAGTG	TGTAGAAACA	AGTAAGGCAG	GTATTAGTAA	2640
TATCAGCTTT	GAGTTTAGCT	CTCTTCGTTT	GTTTATTGCT	GTACCGAAAA	ATCTTCTGTC	2700
TGAGATTGAT	AAAATATCAT	CAAAGGATAT	AGATAACGGG	ATTCATGCTT	TATTTTTTTAA	2760
TTATCAAGTA	AATACAAGGC	TAGCCAATAA	TAAAAATCGT	TATGATTACA	TTTCTGTTTC	2820
ACCAAATATA	AATTATTTTT	CATGGCGGTT	GCGTAATCTT	TTTGAATTTA	ACCAAAACAA	2880
CGATGAAAAA	ACATGGGAAA	GAACTACAC	TTATCTAGAA	AAAAGTTTTT	ATGATAAAAA	2940
GCTAAACTTA	GTCGTTGGTG	AAAGTTATAC	GAATTCAAAT	GTTTATAATA	ACTACTCTTT	3000
TACTGGTATT	TCAGTTTCTA	CAGATACAGA	TATGTATACG	CCAAGTGAAA	TCGATTATAC	3060
ACCAGAAATT	CATGGAGTGG	CTGATTCAGA	CTCTCAGATT	ATTGTCAGGC	AAGGCAACAC	3120

CATTATCATT	AATGAAAGTG	TTCCAGCCGG	ACCGTTCTCA	TTTCCAATAA	CCAATCTCAT	3180
GTATACTGGG	GGGCAACTTA	ATGTGGAGAT	AACAGATATT	TATGGAAATA	AAAAACAATA	3240
TACTGTCAAT	AATTCCTCTC	TTCTGTAT	GAGAAAAGCG	GGACTAATGG	TATATAATTT	3300
TATATCTGGG	AAATTAACAA	AAAAAATAG	TGAGGATGGT	GATTTTTTTA	CTCAAGGTGA	3360
TATTAECTAC	GGTACTCACT	ATAACAGCAC	ACTATTCGGT	GGATATCAGT	TTAGTAAAAA	3420
TTATTTTAAC	TTATCTACTG	GTATAGGCAC	TGATCTGGGA	TTTTCTGGAG	CATGGCTACT	3480
ACACGTTAGC	AGAAGTAATT	TTAAGAATAA	AAATGGATAT	AATATTAATC	TACAACAAAA	3540
CACTCAGTTA	AGACCATTCA	ATGCCGGGGT	TAATTTTCGAT	TACGCATACA	GAAAAAAAAG	3600
GTATGTGGAA	CTTTCCGACA	TTGGCTGGCA	TGGTAATTTA	TATAATCAAC	TTAAAAATAG	3660
TTTTTCTTTA	TCCTTGTCAA	AATCATTGAA	TAAATACGGA	AATTTCTCAC	TTGATTATAA	3720
CAAAATGAAA	TACTGGGATA	ATGCGTATGA	TAGTAACTCA	ATGTCGATTC	GTTATTTTTT	3780
TAAATTCATG	CGAGCAATGA	TTACAACAAA	TTGTTCTTTA	AATAAATATC	AATCTTATGA	3840
AAAAAAGAT	AAAAGATTTA	GTATTAATAT	ATCATTGCCT	TTAACCAAAG	ATTACGGGCA	3900
CATATCTTCA	AACTATTCAT	TTTCCAATGC	AAATACAGGA	ACGGCAACCA	GTTCTGTAGG	3960
CTTAAACGGT	AGTTTTTTTA	ATGACGCAAG	ATTAACTGG	AACATTCAGC	AGAACAGAAC	4020
GACCCGTAAC	AATGGATATA	CTGATAATAC	CAGTTACATA	GCAACCAGCT	ATGCCTCTCC	4080
CTATGGCGTT	TTTACTGGTT	CATATTCAGG	ATCGAACAAG	TATTCAAGCC	AGTTTTATTC	4140
TGCATCGGGA	GGTATTGTTT	TGCATAGCGA	TGGCGTAGCT	TTTACTCAA	AAGCCGGAGA	4200
TACCTCTGCT	CTTGTCGTA	TTGATAATAT	TTCTGATATA	AAAATTGGTA	ACACTCCTGG	4260
TGTTTATACT	GGGTATAATG	GTTTTGCTTT	AATTCCTCAT	CTTCAGCCGT	TCAAAAAAAA	4320
CACCATTTTA	ATTAATGATA	AAGGAATTCC	AGACGGTATT	ACTCTTGCTA	ATATAAAAAA	4380
ACAAGTTATC	CCATCACGAG	GAGCTATTGT	TAAAGTAAAA	TTTGATGCTA	AAAAAGGCAA	4440
TGACATTTTG	TTTAAGCTTA	CAACTAAAGA	TGGAAAAACG	CCCCATTAG	GAGCTATAGC	4500
CCATGAAAAA	AATGGAAAAC	AGATTAATAC	GGGTATCGTT	GACGATGATG	GTATGCTTTA	4560
TATGTCTGGA	TTATCAGGGA	CAGGGATTAT	TAATGTAACA	TGGAATGGAA	AAGTCTGTTC	4620
ATTTCTTTT	TCAGAAAAAG	ATATATCTAG	CAAACAATTA	TCTGTTGTAA	ATAACAATG	4680
TTAGGTAGTG	CATCCAATTA	GTAGAACATG	TGTTTTTCGA	TAAACGCTCC	GATCTCTTTT	4740

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTTAC GAGCCAACCG CTTAATGCGG 4800
GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTTGCC GGTCAGATGC 4860
TTATTCTTCG GTACC 4875

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC

22

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACATT	ACGAATGTTA	TGTATACAAT	AAAAATGATT	ATAGCAATAT	TAATGGTGT	60
ATATGAAGAA	AACAATTGGT	TTAATTCTAA	TTCTTGCTTC	ATTCGGCAGC	CATGCCAGAA	120
CAGAAATAGC	GACTAAAAAC	TTCCCAGTAT	CAACGACTAT	TTCAAAAAGT	TTTTTTGCAC	180
CTGAACCACG	AATACAGCCT	TCTTTTGGTG	AAAATGTTGG	AAAGGAAGGA	GCTTTATTAT	240
TTAGTGTGAA	CTTAACTGTT	CCTGAAAATG	TATCCCAGGT	AACGGTCTAC	CCTGTTTATG	300
ATGAAGATTA	TGGGTTAGGA	CGACTAGTAA	ATACCGCTGA	TGCTTCCCAA	TCAATAATCT	360
ACCAGATTGT	TGATGAGAAA	GGGAAAAAAA	TGTTAAAAGA	TCATGGTGCA	GAGGTTACAC	420
CTAATCAACA	AATAACTTTT	AAAGCGCTGA	ATTATACTAG	CGGGGAAAAA	AAAATATCTC	480
CTGGAATATA	TAACGATCAG	GTTATGGTTG	GTTACTATGT	AAACTAA		527

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Lys	Lys	Thr	Ile	Gly	Leu	Ile	Leu	Ile	Leu	Ala	Ser	Phe	Gly	Ser
1				5				10						15	

His	Ala	Arg	Thr	Glu	Ile	Ala	Thr	Lys	Asn	Phe	Pro	Val	Ser	Thr	Thr
			20					25					30		

Ile	Ser	Lys	Ser	Phe	Phe	Ala	Pro	Glu	Pro	Arg	Ile	Gln	Pro	Ser	Phe
		35					40					45			

Gly	Glu	Asn	Val	Gly	Lys	Glu	Gly	Ala	Leu	Leu	Phe	Ser	Val	Asn	Leu
50						55					60				

Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65 70 75 80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
85 90 95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
100 105 110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
115 120 125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
130 135 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
1 5 10 15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
20 25 30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
35 40 45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
50 55 60

Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
65 70 75 80

Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
85 90 95

Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
100 105 110

Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
115 120 125

Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
130 135 140

Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
145 150 155 160

Thr Val Ser Phe Tyr Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
1 5 10 15

Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
20 25 30

Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
35 40 45

Thr	Pro	Pro	Ile	Phe	Lys	Met	Glu	Ser	Glu	Ser	Arg	Asn	Ile	Ile	Lys	
50						55					60					
Ile	Ile	Lys	Thr	Thr	Ile	Asn	Leu	Pro	Asp	Ser	Gln	Glu	Ser	Met	Arg	
65					70					75					80	
Trp	Leu	Cys	Ile	Glu	Ser	Met	Pro	Pro	Ile	Glu	Lys	Ser	Thr	Lys	Ile	
				85					90					95		
Asn	Arg	Lys	Glu	Gly	Arg	Thr	Asp	Ser	Ile	Asn	Ile	Ser	Ile	Arg	Gly	
			100					105					110			
Cys	Ile	Lys	Leu	Ile	Tyr	Arg	Pro	Ala	Ser	Val	Pro	Ser	Pro	Val	Phe	
		115					120					125				
Asn	Asn	Ile	Val	Glu	Lys	Leu	Lys	Trp	His	Lys	Asn	Gly	Lys	Tyr	Leu	
	130					135					140					
Val	Leu	Lys	Asn	Asn	Thr	Pro	Tyr	Tyr	Ile	Ser	Phe	Ser	Glu	Val	Phe	
145					150					155					160	
Phe	Asp	Ser	Asp	Lys	Val	Asn	Asn	Ala	Lys	Asp	Ile	Leu	Tyr	Val	Lys	
				165					170					175		
Pro	Tyr	Ser	Glu	Lys	Lys	Ile	Asp	Ile	Ser	Asn	Arg	Ile	Ile	Lys	Lys	
			180					185					190			
Ile	Lys	Trp	Ala	Met	Ile	Asp	Asp	Ala	Gly	Ala	Lys	Thr	Lys	Leu	Tyr	
		195					200					205				
Glu	Ser	Ile	Leu													
210																

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Gln Phe Tyr Lys Lys Ser His Tyr Ser Ile Gln Lys His Gln
1 5 10 15

Ile Thr Gly Leu Leu Phe Leu Leu Phe Ile Tyr Pro Phe Ser Thr Ser
20 25 30

Tyr Gly Asn Glu Gln Phe Ser Phe Asp Ser Arg Phe Leu Pro Ser Gly
35 40 45

Tyr Asn Tyr Ser Leu Asn Ser Asn Leu Pro Pro Glu Gly Glu Tyr Leu
50 55 60

Val Asp Ile Tyr Ile Asn Lys Ile Lys Lys Glu Ser Ala Ile Ile Pro
65 70 75 80

Phe Tyr Ile Lys Gly Asn Lys Leu Val Pro Cys Leu Ser Lys Glu Lys
85 90 95

Ile Ser Ser Leu Gly Ile Asn Ile Asn Asn Asp Asn Thr Glu Cys
100 105 110

Val Glu Thr Ser Lys Ala Gly Ile Ser Asn Ile Ser Phe Glu Phe Ser
115 120 125

Ser Leu Arg Leu Phe Ile Ala Val Pro Lys Asn Leu Leu Ser Glu Ile
130 135 140

Asp Lys Ile Ser Ser Lys Asp Ile Asp Asn Gly Ile His Ala Leu Phe
145 150 155 160

Phe Asn Tyr Gln Val Asn Thr Arg Leu Ala Asn Asn Lys Asn Arg Tyr
165 170 175

Asp Tyr Ile Ser Val Ser Pro Asn Ile Asn Tyr Phe Ser Trp Arg Leu
180 185 190

Arg Asn Leu Phe Glu Phe Asn Gln Asn Asn Asp Glu Lys Thr Trp Glu
195 200 205

Arg	Asn	Tyr	Thr	Tyr	Leu	Glu	Lys	Ser	Phe	Tyr	Asp	Lys	Lys	Leu	Asn
	210					215					220				
Leu	Val	Val	Gly	Glu	Ser	Tyr	Thr	Asn	Ser	Asn	Val	Tyr	Asn	Asn	Tyr
225					230					235					240
Ser	Phe	Thr	Gly	Ile	Ser	Val	Ser	Thr	Asp	Thr	Asp	Met	Tyr	Thr	Pro
				245					250					255	
Ser	Glu	Ile	Asp	Tyr	Thr	Pro	Glu	Ile	His	Gly	Val	Ala	Asp	Ser	Asp
			260					265					270		
Ser	Gln	Ile	Ile	Val	Arg	Gln	Gly	Asn	Thr	Ile	Ile	Ile	Asn	Glu	Ser
		275					280					285			
Val	Pro	Ala	Gly	Pro	Phe	Ser	Phe	Pro	Ile	Thr	Asn	Leu	Met	Tyr	Thr
	290					295					300				
Gly	Gly	Gln	Leu	Asn	Val	Glu	Ile	Thr	Asp	Ile	Tyr	Gly	Asn	Lys	Lys
305					310					315					320
Gln	Tyr	Thr	Val	Asn	Asn	Ser	Ser	Leu	Pro	Val	Met	Arg	Lys	Ala	Gly
				325					330					335	
Leu	Met	Val	Tyr	Asn	Phe	Ile	Ser	Gly	Lys	Leu	Thr	Lys	Lys	Asn	Ser
			340					345					350		
Glu	Asp	Gly	Asp	Phe	Phe	Thr	Gln	Gly	Asp	Ile	Asn	Tyr	Gly	Thr	His
		355					360					365			
Tyr	Asn	Ser	Thr	Leu	Phe	Gly	Gly	Tyr	Gln	Phe	Ser	Lys	Asn	Tyr	Phe
	370					375					380				
Asn	Leu	Ser	Thr	Gly	Ile	Gly	Thr	Asp	Leu	Gly	Phe	Ser	Gly	Ala	Trp
385					390					395					400
Leu	Leu	His	Val	Ser	Arg	Ser	Asn	Phe	Lys	Asn	Lys	Asn	Gly	Tyr	Asn
				405					410					415	
Ile	Asn	Leu	Gln	Gln	Asn	Thr	Gln	Leu	Arg	Pro	Phe	Asn	Ala	Gly	Val
			420					425					430		

Asn	Phe	Asp	Tyr	Ala	Tyr	Arg	Lys	Lys	Arg	Tyr	Val	Glu	Leu	Ser	Asp	435	440	445
Ile	Gly	Trp	His	Gly	Asn	Leu	Tyr	Asn	Gln	Leu	Lys	Asn	Ser	Phe	Ser	450	455	460
Leu	Ser	Leu	Ser	Lys	Ser	Leu	Asn	Lys	Tyr	Gly	Asn	Phe	Ser	Leu	Asp	465	470	475
Tyr	Asn	Lys	Met	Lys	Tyr	Trp	Asp	Asn	Ala	Tyr	Asp	Ser	Asn	Ser	Met	485	490	495
Ser	Ile	Arg	Tyr	Phe	Phe	Lys	Phe	Met	Arg	Ala	Met	Ile	Thr	Thr	Asn	500	505	510
Cys	Ser	Leu	Asn	Lys	Tyr	Gln	Ser	Tyr	Glu	Lys	Lys	Asp	Lys	Arg	Phe	515	520	525
Ser	Ile	Asn	Ile	Ser	Leu	Pro	Leu	Thr	Lys	Asp	Tyr	Gly	His	Ile	Ser	530	535	540
Ser	Asn	Tyr	Ser	Phe	Ser	Asn	Ala	Asn	Thr	Gly	Thr	Ala	Thr	Ser	Ser	545	550	555
Val	Gly	Leu	Asn	Gly	Ser	Phe	Phe	Asn	Asp	Ala	Arg	Leu	Asn	Trp	Asn	565	570	575
Ile	Gln	Gln	Asn	Arg	Thr	Thr	Arg	Asn	Asn	Gly	Tyr	Thr	Asp	Asn	Thr	580	585	590
Ser	Tyr	Ile	Ala	Thr	Ser	Tyr	Ala	Ser	Pro	Tyr	Gly	Val	Phe	Thr	Gly	595	600	605
Ser	Tyr	Ser	Gly	Ser	Asn	Lys	Tyr	Ser	Ser	Gln	Phe	Tyr	Ser	Ala	Ser	610	615	620
Gly	Gly	Ile	Val	Leu	His	Ser	Asp	Gly	Val	Ala	Phe	Thr	Gln	Lys	Ala	625	630	635
Gly	Asp	Thr	Ser	Ala	Leu	Val	Arg	Ile	Asp	Asn	Ile	Ser	Asp	Ile	Lys	645	650	655

Ile	Gly	Asn	Thr	Pro	Gly	Val	Tyr	Thr	Gly	Tyr	Asn	Gly	Phe	Ala	Leu
			660					665					670		
Ile	Pro	His	Leu	Gln	Pro	Phe	Lys	Lys	Asn	Thr	Ile	Leu	Ile	Asn	Asp
		675					680					685			
Lys	Gly	Ile	Pro	Asp	Gly	Ile	Thr	Leu	Ala	Asn	Ile	Lys	Lys	Gln	Val
	690					695					700				
Ile	Pro	Ser	Arg	Gly	Ala	Ile	Val	Lys	Val	Lys	Phe	Asp	Ala	Lys	Lys
705					710					715					720
Gly	Asn	Asp	Ile	Leu	Phe	Lys	Leu	Thr	Thr	Lys	Asp	Gly	Lys	Thr	Pro
				725					730					735	
Pro	Leu	Gly	Ala	Ile	Ala	His	Glu	Lys	Asn	Gly	Lys	Gln	Ile	Asn	Thr
			740					745					750		
Gly	Ile	Val	Asp	Asp	Asp	Gly	Met	Leu	Tyr	Met	Ser	Gly	Leu	Ser	Gly
		755					760					765			
Thr	Gly	Ile	Ile	Asn	Val	Thr	Trp	Asn	Gly	Lys	Val	Cys	Ser	Phe	Pro
	770					775					780				
Phe	Ser	Glu	Lys	Asp	Ile	Ser	Ser	Lys	Gln	Leu	Ser	Val	Val	Asn	Lys
785					790					795					800
Gln	Cys														

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
1 5 10 15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
20 25 30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
35 40 45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
50 55 60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
65 70 75 80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
85 90 95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
100 105 110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
115 120 125

Val Met Val Gly Tyr Tyr Val Asn
130 135

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
1 5 10 15

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
20 25 30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
35 40 45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
50 55 60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65 70 75 80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
85 90 95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
100 105 110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
115 120 125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
130 135 140

Ser Asn
145